```
FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 18:25:59 ON
     21 JUN 2006
L1            2 SEA ABB=ON  PLU=ON  CAPSULATUM (20W) (CHITIN (2W) SYNTHASE)
L2            2 DUP REM L1 (0 DUPLICATES REMOVED)
               D L2 BIB ABS 1-2
L3         2949 SEA ABB=ON  PLU=ON  (CHITIN (2W) SYNTHASE)
L4           14 SEA ABB=ON  PLU=ON  L3 AND CAPSULATUM
L5           14 DUP REM L4 (0 DUPLICATES REMOVED)
               D L5 BIB ABS 1-14
L6        28165 SEA ABB=ON  PLU=ON  JOHNSON C?/AU
L7           23 SEA ABB=ON  PLU=ON  L6 AND CAPSULATUM
L8           11 DUP REM L7 (12 DUPLICATES REMOVED)
               D L8 BIB ABS 1-11
L9            0 SEA ABB=ON  PLU=ON  MCEMEN J?/AU
L10        1456 SEA ABB=ON  PLU=ON  MCEWEN J?/AU
L11          37 SEA ABB=ON  PLU=ON  L10 AND CAPSULATUM
L12          16 DUP REM L11 (21 DUPLICATES REMOVED)
               D L12 BIB ABS 1-16
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# EAST Search History

| Ref # | Hits | Search Query | DBs | Default Operator | Plurals | Time Stamp |
|---|---|---|---|---|---|---|
| L1 | 4489 | johnson-c$.in. mcewen-j$.in. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2006/06/21 18:35 |
| L2 | 3 | 1 and capsulatum | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2006/06/21 18:35 |
| L3 | 271 | chitin near2 synthase | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2006/06/21 18:36 |
| L4 | 40 | 3 and capsulatum | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2006/06/21 18:36 |
| L5 | 1 | 3 same capsulatum | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2006/06/21 18:36 |

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on:          May 26, 2006, 04:36:41 ; Search time 2622.09 Seconds
                                            (without alignments)
                                         6853.025 Million cell updates/sec

Title:           US-10-718-955-1
Perfect score:   281
Sequence:        1 gtgagaaaacactctttcct..........tgccccttaaatcgctccag 281


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries

Database :       GenEmbl:*
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                 2:  gb_pat:*
                 3:  gb_ph:*
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                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
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                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
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SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 83.6 | 29.8 | 92585 | 12 | CT033796 | CT033796 Danio rer |
| c | 2 | 82.8 | 29.5 | 362 | 13 | AF359997 | AF359997 Penaeus ( |
| | 3 | 82.2 | 29.3 | 162768 | 12 | AC148720 | AC148720 Ictalurus |
| | 4 | 81.4 | 29.0 | 216720 | 12 | AC112768 | AC112768 Rattus no |
| | 5 | 81.2 | 28.9 | 185946 | 11 | BX548045 | BX548045 Zebrafish |
| c | 6 | 81 | 28.8 | 158797 | 12 | CR854915 | CR854915 Danio rer |
| c | 7 | 81 | 28.8 | 179729 | 11 | BX530035 | BX530035 Zebrafish |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | 8 | 81 | 28.8 | 183364 | 12 | CR933838 | CR933838 Danio rer |
| | 9 | 80.8 | 28.8 | 200882 | 11 | AL953852 | AL953852 Zebrafish |
| c | 10 | 80.6 | 28.7 | 245423 | 12 | AC131848 | AC131848 Rattus no |
| c | 11 | 80.2 | 28.5 | 64433 | 12 | AC131600 | AC131600 Mus muscu |
| c | 12 | 80.2 | 28.5 | 192484 | 6 | AC134906 | AC134906 Mus muscu |
| c | 13 | 80.2 | 28.5 | 195273 | 6 | AC147474 | AC147474 Mus muscu |
| c | 14 | 79.8 | 28.4 | 174999 | 11 | AL840636 | AL840636 Zebrafish |
| c | 15 | 79.8 | 28.4 | 175342 | 11 | AL807799 | AL807799 Zebrafish |
| | 16 | 79.8 | 28.4 | 210873 | 12 | CR391917 | CR391917 Danio rer |
| | 17 | 79.8 | 28.4 | 222137 | 12 | CR954958 | CR954958 Danio rer |
| | 18 | 79.6 | 28.3 | 170260 | 11 | BX908763 | BX908763 Zebrafish |
| c | 19 | 79.6 | 28.3 | 204103 | 11 | BX088705 | BX088705 Zebrafish |
| | 20 | 79.6 | 28.3 | 258612 | 12 | AC095939 | AC095939 Rattus no |
| c | 21 | 79.4 | 28.3 | 155228 | 6 | AC134399 | AC134399 Mus muscu |
| c | 22 | 79.4 | 28.3 | 164878 | 12 | CT025582 | CT025582 Danio rer |
| | 23 | 79.4 | 28.3 | 177877 | 6 | AC163995 | AC163995 Mus muscu |
| c | 24 | 79.4 | 28.3 | 194427 | 6 | AC165080 | AC165080 Mus muscu |
| c | 25 | 79.4 | 28.3 | 203399 | 12 | AC121559 | AC121559 Mus muscu |
| c | 26 | 79.4 | 28.3 | 204468 | 12 | AC165354 | AC165354 Mus muscu |
| c | 27 | 79.2 | 28.2 | 144823 | 11 | BX897744 | BX897744 Zebrafish |
| | 28 | 79.2 | 28.2 | 152517 | 11 | BX927074 | BX927074 Zebrafish |
| | 29 | 79.2 | 28.2 | 196336 | 11 | BX572621 | BX572621 Zebrafish |
| | 30 | 79.2 | 28.2 | 261898 | 12 | CR926458 | CR926458 Danio rer |
| | 31 | 79.2 | 28.2 | 349980 | 2 | CQ870290 | CQ870290 Sequence |
| | 32 | 79 | 28.1 | 142743 | 6 | AL645695 | AL645695 Mouse DNA |
| c | 33 | 79 | 28.1 | 192579 | 12 | AC141584 | AC141584 Rattus no |
| | 34 | 79 | 28.1 | 209713 | 12 | CT027692 | CT027692 Danio rer |
| c | 35 | 78.8 | 28.0 | 85185 | 11 | BX322638 | BX322638 Zebrafish |
| | 36 | 78.8 | 28.0 | 110000 | 4 | AP008211_190 | Continuation (191 |
| | 37 | 78.8 | 28.0 | 136195 | 11 | BX465849 | BX465849 Zebrafish |
| | 38 | 78.8 | 28.0 | 143739 | 4 | AC132483 | AC132483 Oryza sat |
| | 39 | 78.8 | 28.0 | 160405 | 11 | BX510999 | BX510999 Zebrafish |
| | 40 | 78.8 | 28.0 | 161346 | 11 | BX511013 | BX511013 Zebrafish |
| c | 41 | 78.8 | 28.0 | 192541 | 6 | AC153502 | AC153502 Mus muscu |
| c | 42 | 78.6 | 28.0 | 115973 | 12 | CT573113 | CT573113 Danio rer |
| | 43 | 78.6 | 28.0 | 149928 | 12 | AC134950 | AC134950 Danio rer |
| c | 44 | 78.6 | 28.0 | 154856 | 12 | AC119792 | AC119792 Rattus no |
| c | 45 | 78.6 | 28.0 | 156284 | 11 | AL929336 | AL929336 Zebrafish |
| c | 46 | 78.6 | 28.0 | 179154 | 12 | AC141487 | AC141487 Rattus no |
| | 47 | 78.6 | 28.0 | 188859 | 11 | BX247903 | BX247903 Zebrafish |
| c | 48 | 78.6 | 28.0 | 192603 | 11 | BX323087 | BX323087 Zebrafish |
| | 49 | 78.6 | 28.0 | 196462 | 12 | CT025856 | CT025856 Danio rer |
| c | 50 | 78.6 | 28.0 | 203466 | 6 | AC162920 | AC162920 Mus muscu |
| c | 51 | 78.4 | 27.9 | 162206 | 12 | CR926911 | CR926911 Danio rer |
| c | 52 | 78.4 | 27.9 | 241995 | 12 | AC097900 | AC097900 Rattus no |
| | 53 | 78.4 | 27.9 | 245166 | 12 | AC107262 | AC107262 Rattus no |
| | 54 | 78.2 | 27.8 | 120558 | 11 | CR450689 | CR450689 Zebrafish |
| | 55 | 78.2 | 27.8 | 186106 | 12 | BX088565 | BX088565 Danio rer |
| c | 56 | 78.2 | 27.8 | 186318 | 11 | BX119930 | BX119930 Zebrafish |
| c | 57 | 78.2 | 27.8 | 191281 | 11 | AL935185 | AL935185 Zebrafish |
| c | 58 | 78.2 | 27.8 | 191781 | 11 | BX000480 | BX000480 Zebrafish |
| | 59 | 78.2 | 27.8 | 204383 | 12 | CR854910 | CR854910 Danio rer |
| | 60 | 78.2 | 27.8 | 232104 | 11 | CR457452 | CR457452 Zebrafish |
| c | 61 | 78 | 27.8 | 122188 | 12 | CT009763 | CT009763 Danio rer |
| | 62 | 78 | 27.8 | 129787 | 12 | CR926460 | CR926460 Danio rer |
| c | 63 | 78 | 27.8 | 144640 | 11 | CR847530 | CR847530 Zebrafish |
| c | 64 | 78 | 27.8 | 145320 | 11 | CR381553 | CR381553 Zebrafish |
| | 65 | 78 | 27.8 | 154419 | 11 | BX957287 | BX957287 Zebrafish |
| | 66 | 78 | 27.8 | 155366 | 11 | BX294662 | BX294662 Zebrafish |
| c | 67 | 78 | 27.8 | 170622 | 12 | CR932359 | CR932359 Danio rer |
| c | 68 | 78 | 27.8 | 171493 | 11 | BX649575 | BX649575 Zebrafish |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| c | 69 | 78 | 27.8 | 174986 | 11 | AL935126 | AL935126 Zebrafish |
| | 70 | 78 | 27.8 | 177516 | 11 | BX294164 | BX294164 Zebrafish |
| | 71 | 78 | 27.8 | 180836 | 12 | CR925859 | CR925859 Danio rer |
| | 72 | 78 | 27.8 | 183380 | 11 | BX469930 | BX469930 Zebrafish |
| | 73 | 78 | 27.8 | 186123 | 11 | BX640592 | BX640592 Zebrafish |
| c | 74 | 78 | 27.8 | 189108 | 6 | AC119242 | AC119242 Mus muscu |
| | 75 | 78 | 27.8 | 198900 | 11 | BX470185 | BX470185 Zebrafish |
| | 76 | 78 | 27.8 | 202348 | 6 | AC154308 | AC154308 Mus muscu |
| c | 77 | 78 | 27.8 | 206857 | 6 | AC152959 | AC152959 Mus muscu |
| | 78 | 78 | 27.8 | 209195 | 11 | AL954309 | AL954309 Zebrafish |
| c | 79 | 78 | 27.8 | 216418 | 12 | CR354597 | CR354597 Danio rer |
| c | 80 | 78 | 27.8 | 230233 | 6 | CT009702 | CT009702 Mouse DNA |
| | 81 | 78 | 27.8 | 311860 | 12 | BX537353 | BX537353 Danio rer |
| | 82 | 77.8 | 27.7 | 138341 | 11 | AL935053 | AL935053 Zebrafish |
| c | 83 | 77.8 | 27.7 | 174828 | 11 | CR352326 | CR352326 Zebrafish |
| c | 84 | 77.8 | 27.7 | 264976 | 12 | AC132800 | AC132800 Rattus no |
| | 85 | 77.6 | 27.6 | 154017 | 11 | CR774185 | CR774185 Zebrafish |
| c | 86 | 77.6 | 27.6 | 162570 | 11 | BX927311 | BX927311 Zebrafish |
| c | 87 | 77.6 | 27.6 | 167004 | 11 | AL954840 | AL954840 Zebrafish |
| | 88 | 77.6 | 27.6 | 189417 | 6 | BX000995 | BX000995 Mouse DNA |
| c | 89 | 77.6 | 27.6 | 201139 | 12 | AC110548 | AC110548 Mus muscu |
| | 90 | 77.6 | 27.6 | 202346 | 6 | AC121523 | AC121523 Mus muscu |
| | 91 | 77.4 | 27.5 | 140087 | 12 | CR931815 | CR931815 Danio rer |
| c | 92 | 77.4 | 27.5 | 172954 | 11 | AL929152 | AL929152 Zebrafish |
| | 93 | 77.4 | 27.5 | 190385 | 12 | CT573411 | CT573411 Danio rer |
| | 94 | 77.4 | 27.5 | 236418 | 12 | CR318626 | CR318626 Danio rer |
| c | 95 | 77.2 | 27.5 | 47439 | 11 | BX901875 | BX901875 Zebrafish |
| c | 96 | 77.2 | 27.5 | 139220 | 11 | CR936460 | CR936460 Zebrafish |
| | 97 | 77.2 | 27.5 | 141291 | 6 | AC157092 | AC157092 Mus muscu |
| | 98 | 77.2 | 27.5 | 208710 | 6 | AC118200 | AC118200 Mus muscu |
| | 99 | 77.2 | 27.5 | 222615 | 12 | AC121379 | AC121379 Rattus no |

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          GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on:           May 26, 2006, 04:26:31 ; Search time 945.656 Seconds
                                            (without alignments)
                                           2071.790 Million cell updates/sec


Title:            US-10-718-955-1
Perfect score:    281
Sequence:         1 gtgagaaaacactctttcct..........tgccccttaaatcgctccag 281


Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0


Searched:         5244920 seqs, 3486124231 residues


Total number of hits satisfying chosen parameters:       10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries


Database :        N_Geneseq_8:*
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                  2:  geneseqn1990s:*
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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.


                                  SUMMARIES
                       %
Result               Query
   No.     Score   Match  Length DB   ID                     Description
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c   1      82.8     29.5     926  3   ABN81102               Abn81102 Shrimp po
    2      79.2     28.2  110000 13   ABD32966_02            Continuation (3 of
c   3      78.6     28.0  261066 14   AEE04993               Aee04993 Cancer-as
    4      71.8     25.6  111206 11   ACN45152               Acn45152 Mouse gen
    5      71.2     25.3  242496 14   AED76150               Aed76150 Mouse CA
    6      70.6     25.1  138627 12   ADQ97183               Adq97183 Human can
    7      70.2     25.0  110000 15   AEF10213_0             Aef10213 Human pro
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|   |    |      |      |        |    |            |                        |
|---|----|------|------|--------|----|------------|------------------------|
|   | 8  | 70.2 | 25.0 | 260160 | 12 | ADQ20017   | Adq20017 Human sof     |
|   | 9  | 69.4 | 24.7 | 70215  | 11 | ACN43992   | Acn43992 Mouse gen     |
|   | 10 | 68.8 | 24.5 | 235962 | 14 | ADZ12926   | Adz12926 Murine ca     |
| c | 11 | 67.6 | 24.1 | 46456  | 9  | ADA02825   | Ada02825 Mouse Pou     |
| c | 12 | 67.6 | 24.1 | 46456  | 10 | ADB72563   | Adb72563 Mouse Pou     |
| c | 13 | 67.6 | 24.1 | 46456  | 12 | ADM74420   | Adm74420 Murine ca     |
| c | 14 | 67.6 | 24.1 | 46458  | 10 | ADC85304   | Adc85304 Human Sos     |
| c | 15 | 67.2 | 23.9 | 96599  | 9  | ADA02747   | Ada02747 Mouse Irf     |
| c | 16 | 67.2 | 23.9 | 96599  | 10 | ADB72485   | Adb72485 Mouse Irf     |
| c | 17 | 67.2 | 23.9 | 96599  | 10 | ADC85227   | Adc85227 Mouse Irf     |
| c | 18 | 67.2 | 23.9 | 96599  | 12 | ADM74342   | Adm74342 Murine ca     |
|   | 19 | 65.6 | 23.3 | 261817 | 11 | ACN45182   | Acn45182 Human gen     |
|   | 20 | 64.4 | 22.9 | 31277  | 11 | ACN44854   | Acn44854 Human gen     |
| c | 21 | 64.4 | 22.9 | 126488 | 14 | ADZ12943   | Adz12943 Human can     |
|   | 22 | 64   | 22.8 | 123192 | 13 | ADV34995   | Adv34995 Murine cD     |
|   | 23 | 64   | 22.8 | 155350 | 13 | ABD33514   | Abd33514 Murine ca     |
|   | 24 | 63.8 | 22.7 | 134000 | 14 | AED76160   | Aed76160 Mouse CA      |
|   | 25 | 63.6 | 22.6 | 54810  | 13 | ABD32759   | Abd32759 Mouse can     |
|   | 26 | 63.6 | 22.6 | 79544  | 12 | ADQ97764   | Adq97764 Human can     |
| c | 27 | 63.2 | 22.5 | 198522 | 11 | ACN44010   | Acn44010 Human gen     |
|   | 28 | 63   | 22.4 | 2983   | 4  | AAK83652   | Aak83652 Human imm     |
|   | 29 | 63   | 22.4 | 15698  | 6  | ABL34141   | Abl34141 Human imm     |
| c | 30 | 63   | 22.4 | 89824  | 13 | ABD32895   | Abd32895 Mouse can     |
|   | 31 | 62.8 | 22.3 | 256493 | 11 | ACN44514   | Acn44514 Human gen     |
| c | 32 | 62.6 | 22.3 | 42611  | 10 | ABV75791   | Abv75791 Human lip     |
| c | 33 | 62.6 | 22.3 | 43672  | 11 | ACN44252   | Acn44252 Mouse gen     |
|   | 34 | 62.6 | 22.3 | 117962 | 8  | AAD54480   | Aad54480 Human CIP     |
|   | 35 | 62.6 | 22.3 | 227968 | 6  | ABK83497   | Abk83497 Human cDN     |
|   | 36 | 62.6 | 22.3 | 227968 | 12 | ADQ18538   | Adq18538 Human sof     |
|   | 37 | 62.6 | 22.3 | 227968 | 14 | AED17856   | Aed17856 Fibrotic      |
| c | 38 | 62.4 | 22.2 | 196063 | 13 | ABD33462   | Abd33462 Human can     |
| c | 39 | 61.8 | 22.0 | 141463 | 11 | ACN43862   | Acn43862 Human gen     |
|   | 40 | 61.4 | 21.9 | 87468  | 15 | AEF10213_3 | Continuation (4 of     |
|   | 41 | 61   | 21.7 | 2889   | 4  | AAK83654   | Aak83654 Human imm     |
|   | 42 | 61   | 21.7 | 6727   | 2  | AAT88014   | Aat88014 Murine IL     |
|   | 43 | 61   | 21.7 | 6727   | 3  | AAC73648   | Aac73648 Murine IL     |
|   | 44 | 61   | 21.7 | 6727   | 8  | ABX04302   | Abx04302 Mouse Int     |
|   | 45 | 61   | 21.7 | 6727   | 12 | ADR11979   | Adr11979 Murine in     |
| c | 46 | 61   | 21.7 | 11112  | 6  | ABQ72905   | Abq72905 Human GRM     |
| c | 47 | 61   | 21.7 | 11112  | 6  | ABQ72798   | Abq72798 Human GRM     |
|   | 48 | 61   | 21.7 | 48133  | 11 | ACN44860   | Acn44860 Mouse gen     |
| c | 49 | 60.8 | 21.6 | 36221  | 10 | ADH63075   | Adh63075 Human fib     |
|   | 50 | 60.8 | 21.6 | 110000 | 12 | ADQ97050_2 | Continuation (3 of     |
| c | 51 | 60.6 | 21.6 | 7576   | 12 | ADM67662   | Adm67662 Rice Ehd1     |
|   | 52 | 60.6 | 21.6 | 210528 | 11 | ACN44040   | Acn44040 Mouse gen     |
|   | 53 | 60.4 | 21.5 | 26997  | 4  | AAS46748   | Aas46748 Tumour su     |
| c | 54 | 60.2 | 21.4 | 110000 | 13 | ABD32966_07| Continuation (8 of     |
| c | 55 | 60   | 21.4 | 110000 | 13 | ABD32966_06| Continuation (7 of     |
|   | 56 | 59.8 | 21.3 | 1807   | 13 | ADR07494   | Adr07494 Full leng     |
| c | 57 | 59.8 | 21.3 | 110000 | 12 | ADN97989_13| Continuation (14 o     |
|   | 58 | 59.8 | 21.3 | 110000 | 14 | ADZ46976_0 | Adz46976 Human pho     |
| c | 59 | 59.8 | 21.3 | 304326 | 13 | ADS15253   | Ads15253 Rat senso     |
|   | 60 | 59.6 | 21.2 | 6621   | 6  | ABK33932   | Abk33932 Human DNA     |
|   | 61 | 59.6 | 21.2 | 6621   | 6  | ABL70155   | Abl70155 Chemicall     |
|   | 62 | 59.6 | 21.2 | 6621   | 6  | AAS61097   | Aas61097 Human gen     |
|   | 63 | 59.6 | 21.2 | 6621   | 8  | ABZ09983   | Abz09983 Haematopo     |
|   | 64 | 59.6 | 21.2 | 6621   | 8  | ABZ10129   | Abz10129 Haematopo     |
|   | 65 | 59.6 | 21.2 | 6621   | 8  | ABZ10097   | Abz10097 Haematopo     |
|   | 66 | 59.6 | 21.2 | 6621   | 8  | ABZ10243   | Abz10243 Haematopo     |
|   | 67 | 59.6 | 21.2 | 6621   | 8  | ADA20344   | Ada20344 Prostate      |
|   | 68 | 59.6 | 21.2 | 6621   | 8  | ADA84151   | Ada84151 Human ren     |

|   |    |      |      |        |    |             |                      |
|---|----|------|------|--------|----|-------------|----------------------|
|   | 69 | 59.6 | 21.2 |   6621 | 10 | ADE84153    | Ade84153 Human lym   |
|   | 70 | 59.6 | 21.2 |   6621 | 10 | ADE84077    | Ade84077 Human lym   |
| c | 71 | 59.6 | 21.2 |   7204 |  2 | AAX23527    | Aax23527 O. longis   |
| c | 72 | 59.6 | 21.2 | 104932 | 14 | AEB96542    | Aeb96542 Human STA   |
| c | 73 | 59.6 | 21.2 | 110000 | 14 | AED76254_06 | Continuation (7 of   |
| c | 74 | 59.4 | 21.1 |   3442 | 10 | ADB58100    | Adb58100 Toxicity-   |
|   | 75 | 59.4 | 21.1 |  11745 |  6 | ABK28331    | Abk28331 DNA trans   |
| c | 76 | 59.2 | 21.1 | 110021 | 13 | ABD32859    | Abd32859 Mouse can   |
|   | 77 | 59.2 | 21.1 | 119057 | 13 | ABD33460    | Abd33460 Murine ca   |
| c | 78 | 59.2 | 21.1 | 219715 | 13 | ABD32692    | Abd32692 Mouse can   |
|   | 79 |   59 | 21.0 |   2551 |  2 | AAT30738    | Aat30738 Rat crypt   |
| c | 80 |   59 | 21.0 |   4559 |  4 | AAH27886    | Aah27886 Nucleotid   |
|   | 81 |   59 | 21.0 |  12069 |  6 | ABK39931    | Abk39931 Human che   |
|   | 82 |   59 | 21.0 |  32185 | 11 | ACN44604    | Acn44604 Mouse gen   |
|   | 83 |   59 | 21.0 | 289106 | 14 | ADZ12614    | Adz12614 Murine ca   |
|   | 84 |   59 | 21.0 | 326014 |  6 | ABK89296    | Abk89296 Human gen   |
|   | 85 |   59 | 21.0 | 326014 | 12 | ADQ94981    | Adq94981 Human kin   |
| c | 86 | 58.8 | 20.9 |   3354 | 14 | ADZ70903    | Adz70903 Human mat   |
|   | 87 | 58.8 | 20.9 |  22461 | 14 | AED76280    | Aed76280 Mouse CA    |
|   | 88 | 58.8 | 20.9 | 135652 | 14 | AEE05069    | Aee05069 Cancer-as   |
| c | 89 | 58.6 | 20.9 |  13217 |  4 | AAS35088    | Aas35088 DNA #38 e   |
|   | 90 | 58.6 | 20.9 |  13217 |  4 | AAS31477    | Aas31477 Human DNA   |
| c | 91 | 58.6 | 20.9 |  13217 |  4 | AAI63997    | Aai63997 Human pol   |
| c | 92 | 58.6 | 20.9 |  13217 |  4 | ABA06818    | Aba06818 Human gen   |
| c | 93 | 58.6 | 20.9 |  13217 |  5 | ABA18587    | Aba18587 Human ner   |
| c | 94 | 58.6 | 20.9 |  13217 |  5 | AAS29749    | Aas29749 Human end   |
|   | 95 | 58.6 | 20.9 |  13217 |  6 | ABQ66801    | Abq66801 Human pol   |
| c | 96 | 58.6 | 20.9 |  13217 |  6 | ABV84155    | Abv84155 Human pol   |
|   | 97 | 58.6 | 20.9 |  13217 | 10 | ADC11088    | Adc11088 Human DNA   |
| c | 98 | 58.6 | 20.9 |  13217 | 10 | ADC46530    | Adc46530 Human neo   |
| c | 99 | 58.6 | 20.9 |  13217 | 12 | ADM24712    | Adm24712 Human PRO   |

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   GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on:          May 26, 2006, 04:56:26 ; Search time 268.82 Seconds
                                              (without alignments)
                                           1955.884 Million cell updates/sec


Title:           US-10-718-955-1
Perfect score:   281
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        1403666 seqs, 935554401 residues


Total number of hits satisfying chosen parameters:      2807332


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries


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      Pred. No. is the number of results predicted by chance to have a
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|  | 7 | 64.2 | 22.8 | 767677 | 3 | US-09-949-016-17361 | Sequence 17361, A |
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| c | 9 | 63.8 | 22.7 | 601 | 3 | US-09-949-016-198481 | Sequence 198481, |
| c | 10 | 63.4 | 22.6 | 16434 | 3 | US-09-949-016-13235 | Sequence 13235, A |
| c | 11 | 63.4 | 22.6 | 26831 | 3 | US-09-949-016-16250 | Sequence 16250, A |
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|   | 17 | 60.8 | 21.6 | 670690 | 3 | US-09-949-016-14207   | Sequence 14207, A    |
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|   | 33 | 57   | 20.3 | 601    | 3 | US-09-949-016-31837   | Sequence 31837, A    |
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|   | 79 | 54.8 | 19.5 | 69813 | 3 | US-09-949-016-12455 | Sequence 12455, A |
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| c | 100 | 54.2 | 19.3 | 52202 | 3 | US-09-949-016-17006 | Sequence 17006, A |

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OM nucleic - nucleic search, using sw model

Run on:              May 26, 2006, 05:16:51 ; Search time 1776.48 Seconds
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Scoring table:       IDENTITY_NUC
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Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a
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| c 3 | 71.6 | 25.5 | 59247 | 8 | US-10-741-601-5741 | Sequence 5741, Ap |
| c 4 | 71.6 | 25.5 | 59247 | 9 | US-10-741-600-17890 | Sequence 17890, A |
| 5 | 71.6 | 25.5 | 161700 | 8 | US-10-741-601-5623 | Sequence 5623, Ap |
| 6 | 71.6 | 25.5 | 161700 | 9 | US-10-741-600-17590 | Sequence 17590, A |

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|   | 10 | 71   | 25.3 | 535    | 12 | US-10-301-480-755003   | Sequence 755003,      |
|   | 11 | 70.6 | 25.1 | 138627 | 11 | US-10-330-773-159      | Sequence 159, App     |
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    GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

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                 Listing first 600 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result              Query
   No.     Score   Match Length DB  ID                      Description
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      1     50.2   17.9    2798  7  US-11-145-307A-179       Sequence 179, App
      2     49     17.4     506  6  US-10-488-619-2562       Sequence 2562, Ap
      3     48.8   17.4    2522  7  US-11-293-697-543        Sequence 543, App
  c   4     46.2   16.4    2333  7  US-11-293-697-2386       Sequence 2386, Ap
      5     44.2   15.7    3229  7  US-11-293-697-817        Sequence 817, App
      6     43.6   15.5   42999  7  US-11-284-877-17         Sequence 17, Appl
  c   7     43.2   15.4    1235  6  US-10-953-349-16337      Sequence 16337, A
      8     43.2   15.4  151830  6  US-10-519-335-37         Sequence 37, Appl
  c   9     41.8   14.9    2856  7  US-11-293-697-1116       Sequence 1116, Ap
     10     41.6   14.8    6243  6  US-10-518-039-2          Sequence 2, Appli
     11     41.6   14.8    6843  6  US-10-518-039-1          Sequence 1, Appli
     12     41.6   14.8  394191  6  US-10-506-549-3          Sequence 3, Appli
     13     41.4   14.7     342  7  US-11-217-529-80228      Sequence 80228, A
     14     40     14.2    1235  6  US-10-953-349-16337      Sequence 16337, A
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|   | 15 | 40   | 14.2 | 3335   | 7 | US-11-293-697-1050   | Sequence 1050, Ap   |
|   | 16 | 40   | 14.2 | 70665  | 6 | US-10-505-928-596    | Sequence 596, App   |
|   | 17 | 39.8 | 14.2 | 2523   | 7 | US-11-293-697-1322   | Sequence 1322, Ap   |
| c | 18 | 38.8 | 13.8 | 50000  | 6 | US-10-528-659-2      | Sequence 2, Appli   |
|   | 19 | 38.6 | 13.7 | 1989   | 7 | US-11-293-697-362    | Sequence 362, App   |
| c | 20 | 38.6 | 13.7 | 2307   | 7 | US-11-293-697-1429   | Sequence 1429, Ap   |
|   | 21 | 38.4 | 13.7 | 1174   | 6 | US-10-953-349-2820   | Sequence 2820, Ap   |
| c | 22 | 38.2 | 13.6 | 2567   | 6 | US-10-196-749-179    | Sequence 179, App   |
| c | 23 | 38   | 13.5 | 857    | 6 | US-10-953-349-32928  | Sequence 32928, A   |
|   | 24 | 37.6 | 13.4 | 534    | 6 | US-10-505-928-2      | Sequence 2, Appli   |
| c | 25 | 37.6 | 13.4 | 1733   | 7 | US-11-293-697-1577   | Sequence 1577, Ap   |
| c | 26 | 37.4 | 13.3 | 54550  | 7 | US-11-318-813-42     | Sequence 42, Appl   |
|   | 27 | 36.8 | 13.1 | 1538   | 6 | US-10-953-349-17700  | Sequence 17700, A   |
|   | 28 | 36.6 | 13.0 | 658    | 6 | US-10-511-937-570    | Sequence 570, App   |
| c | 29 | 36.6 | 13.0 | 1538   | 6 | US-10-953-349-17700  | Sequence 17700, A   |
| c | 30 | 36.6 | 13.0 | 1623   | 7 | US-11-274-768A-1     | Sequence 1, Appli   |
|   | 31 | 36.2 | 12.9 | 1631   | 7 | US-11-293-697-1928   | Sequence 1928, Ap   |
|   | 32 | 36.2 | 12.9 | 2460   | 7 | US-11-293-697-595    | Sequence 595, App   |
| c | 33 | 36.2 | 12.9 | 70665  | 6 | US-10-505-928-596    | Sequence 596, App   |
| c | 34 | 36.2 | 12.9 | 128361 | 6 | US-10-505-928-151    | Sequence 151, App   |
|   | 35 | 36.2 | 12.9 | 135090 | 6 | US-10-505-928-607    | Sequence 607, App   |
| c | 36 | 36   | 12.8 | 381    | 7 | US-11-217-529-166545 | Sequence 166545,    |
| c | 37 | 36   | 12.8 | 543    | 6 | US-10-488-619-2662   | Sequence 2662, Ap   |
|   | 38 | 36   | 12.8 | 2638   | 6 | US-10-473-173-82     | Sequence 82, Appl   |
| c | 39 | 36   | 12.8 | 2798   | 7 | US-11-145-307A-179   | Sequence 179, App   |
|   | 40 | 35.8 | 12.7 | 2025   | 6 | US-10-511-937-414    | Sequence 414, App   |
|   | 41 | 35.8 | 12.7 | 2681   | 7 | US-11-145-307A-194   | Sequence 194, App   |
| c | 42 | 35.8 | 12.7 | 135090 | 6 | US-10-505-928-607    | Sequence 607, App   |
| c | 43 | 35.8 | 12.7 | 151830 | 6 | US-10-519-335-37     | Sequence 37, Appl   |
|   | 44 | 35.6 | 12.7 | 857    | 6 | US-10-953-349-32928  | Sequence 32928, A   |
| c | 45 | 35.6 | 12.7 | 3121   | 7 | US-11-293-697-1532   | Sequence 1532, Ap   |
| c | 46 | 35.6 | 12.7 | 42999  | 7 | US-11-284-877-17     | Sequence 17, Appl   |
|   | 47 | 35.4 | 12.6 | 1152   | 6 | US-10-953-349-20671  | Sequence 20671, A   |
| c | 48 | 35.4 | 12.6 | 1997   | 7 | US-11-293-697-77     | Sequence 77, Appl   |
| c | 49 | 35.4 | 12.6 | 2628   | 7 | US-11-264-784-50     | Sequence 50, Appl   |
| c | 50 | 35.2 | 12.5 | 2522   | 7 | US-11-293-697-543    | Sequence 543, App   |

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OM nucleic - nucleic search, using sw model

Run on:            May 26, 2006, 04:39:39 ; Search time 6082.82 Seconds
                                             (without alignments)
                                             2583.230 Million cell updates/sec

Title:             US-10-718-955-1
Perfect score:     281
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Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0


Searched:          48236798 seqs, 27959665780 residues


Total number of hits satisfying chosen parameters:        96473596


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries


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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
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SUMMARIES

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| c 2 | 77.6 | 27.6 | 692 | 11 | AZ717324 | AZ717324 RPCI-24-1 |
| c 3 | 76.4 | 27.2 | 406 | 14 | BX129078 | BX129078 Danio rer |
| c 4 | 76.4 | 27.2 | 452 | 14 | BX173084 | BX173084 Danio rer |
| c 5 | 76 | 27.0 | 278 | 11 | BZ252092 | BZ252092 CH230-306 |
| c 6 | 75.4 | 26.8 | 684 | 14 | BX192398 | BX192398 Danio rer |
| c 7 | 75.2 | 26.8 | 191 | 11 | AZ398168 | AZ398168 1M0163P19 |
| 8 | 75.2 | 26.8 | 538 | 14 | DU976720 | DU976720 AUAC-aaa0 |

| | | | | | | | | |
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| c | 9 | 75 | 26.7 | 790 | 11 | BZ141728 | BZ141728 CH230-412 |
| c | 10 | 74.8 | 26.6 | 639 | 14 | BX129734 | BX129734 Danio rer |
| c | 11 | 74.2 | 26.4 | 1014 | 14 | CR133160 | CR133160 Forward s |
| c | 12 | 74 | 26.3 | 598 | 11 | BZ143438 | BZ143438 CH230-462 |
| c | 13 | 74 | 26.3 | 811 | 14 | BX179405 | BX179405 Danio rer |
| c | 14 | 73.8 | 26.3 | 610 | 14 | BX198092 | BX198092 Danio rer |
| | 15 | 73.6 | 26.2 | 585 | 14 | BX186102 | BX186102 Danio rer |
| c | 16 | 73.6 | 26.2 | 757 | 14 | AG607861 | AG607861 Mus muscu |
| c | 17 | 72.8 | 25.9 | 596 | 14 | BX176148 | BX176148 Danio rer |
| c | 18 | 72.8 | 25.9 | 812 | 14 | BX171590 | BX171590 Danio rer |
| c | 19 | 72.4 | 25.8 | 494 | 4 | CB713530 | CB713530 AMGNNUC:M |
| c | 20 | 72.2 | 25.7 | 680 | 14 | BX155076 | BX155076 Danio rer |
| c | 21 | 72.2 | 25.7 | 816 | 14 | BX221269 | BX221269 Danio rer |
| | 22 | 72 | 25.6 | 560 | 11 | AQ981373 | AQ981373 RPCI-23-2 |
| c | 23 | 72 | 25.6 | 648 | 11 | AZ351589 | AZ351589 1M0089P10 |
| c | 24 | 72 | 25.6 | 706 | 11 | AZ947453 | AZ947453 2M0210J12 |
| c | 25 | 71.8 | 25.6 | 613 | 14 | BX157604 | BX157604 Danio rer |
| c | 26 | 71.6 | 25.5 | 269 | 13 | CL791416 | CL791416 OR_BBa011 |
| | 27 | 71.6 | 25.5 | 648 | 14 | BX146163 | BX146163 Danio rer |
| c | 28 | 71.2 | 25.3 | 628 | 7 | BF471856 | BF471856 UI-M-BH3- |
| c | 29 | 71.2 | 25.3 | 730 | 14 | AG383946 | AG383946 Mus muscu |
| c | 30 | 71.2 | 25.3 | 751 | 14 | AG474516 | AG474516 Mus muscu |
| c | 31· | 71.2 | 25.3 | 807 | 11 | AQ914771 | AQ914771 nbeb0049J |
| c | 32 | 71.2 | 25.3 | 1745 | 2 | BM415113 | BM415113 OP20184 M |
| | 33 | 71 | 25.3 | 342 | 14 | BX239094 | BX239094 Danio rer |
| c | 34 | 71 | 25.3 | 729 | 14 | AG463074 | AG463074 Mus muscu |
| c | 35 | 70.8 | 25.2 | 334 | 14 | CR177502 | CR177502 Forward s |
| | 36 | 70.8 | 25.2 | 436 | 14 | BX154558 | BX154558 Danio rer |
| c | 37 | 70.8 | 25.2 | 533 | 11 | BH105130 | BH105130 RPCI-24-4 |
| c | 38 | 70.6 | 25.1 | 206 | 14 | DR30I13S | AL740566 Danio rer |
| c | 39 | 70.6 | 25.1 | 215 | 14 | DR5L17S | AL733845 Danio rer |
| c | 40 | 70.6 | 25.1 | 605 | 14 | BX218654 | BX218654 Danio rer |
| | 41 | 70.6 | 25.1 | 788 | 14 | BX175098 | BX175098 Danio rer |
| c | 42 | 70.2 | 25.0 | 789 | 14 | BX159146 | BX159146 Danio rer |
| c | 43 | 70 | 24.9 | 350 | 14 | DR25B24T | AL982993 Danio rer |
| | 44 | 70 | 24.9 | 510 | 14 | BX183288 | BX183288 Danio rer |
| | 45 | 70 | 24.9 | 592 | 14 | BX180548 | BX180548 Danio rer |
| c | 46 | 70 | 24.9 | 715 | 10 | DW283382 | DW283382 UI-S-HHO- |
| c | 47 | 70 | 24.9 | 730 | 14 | AG610770 | AG610770 Mus muscu |
| c | 48 | 70 | 24.9 | 898 | 11 | BZ122720 | BZ122720 CH230-461 |
| | 49 | 69.8 | 24.8 | 447 | 14 | BX141934 | BX141934 Danio rer |
| | 50 | 69.8 | 24.8 | 572 | 13 | CL989749 | CL989749 ZMMBHe000 |

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         .

OM nucleic - nucleic search, using sw model

Run on:            May 26, 2006, 04:36:41 ; Search time 195.957 Seconds
                                           (without alignments)
                                           6853.025 Million cell updates/sec

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Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:        12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

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c   3    18.4     87.6   37480  12  AC137812                AC137812 Homo sapi
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    5    18.4     87.6  110000  12  AC139250_0              AC139250 Homo sapi
    6    18.4     87.6  110000  15  AE000657_01             Continuation (2 of
    7    18.4     87.6  148252  12  AC135789                AC135789 Homo sapi

| | | | | | | | |
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| c | 8 | 18.4 | 87.6 | 157233 | 5 | AC087564 | AC087564 Homo sapi |
| c | 9 | 18.4 | 87.6 | 167662 | 12 | AC135788 | AC135788 Homo sapi |
| c | 10 | 18.4 | 87.6 | 210697 | 12 | AC135790 | AC135790 Homo sapi |
| | 11 | 18 | 85.7 | 78531 | 12 | AC175508 | AC175508 Bos tauru |
| | 12 | 18 | 85.7 | 159934 | 5 | AC097657 | AC097657 Homo sapi |
| | 13 | 18 | 85.7 | 167796 | 12 | AC109819 | AC109819 Homo sapi |
| c | 14 | 18 | 85.7 | 204190 | 12 | AC140696 | AC140696 Rattus no |
| | 15 | 18 | 85.7 | 279534 | 12 | AC114035 | AC114035 Rattus no |
| c | 16 | 17.8 | 84.8 | 3253 | 11 | BC094173 | BC094173 Xenopus l |
| c | 17 | 17.8 | 84.8 | 110000 | 4 | AP008208_033 | Continuation (34 o |
| c | 18 | 17.8 | 84.8 | 110000 | 12 | AC091229_02 | Continuation (3 of |
| | 19 | 17.8 | 84.8 | 110000 | 12 | AC091242_0 | AC091242 Rattus no |
| | 20 | 17.8 | 84.8 | 110000 | 12 | BX004982_2 | Continuation (3 of |
| | 21 | 17.8 | 84.8 | 110000 | 15 | AE016879_32 | Continuation (33 o |
| | 22 | 17.8 | 84.8 | 110000 | 15 | AE017225_32 | Continuation (33 o |
| | 23 | 17.8 | 84.8 | 110000 | 15 | AE017334_32 | Continuation (33 o |
| c | 24 | 17.8 | 84.8 | 111994 | 11 | CR392352 | CR392352 Zebrafish |
| c | 25 | 17.8 | 84.8 | 119844 | 12 | AC158446 | AC158446 Loxodonta |
| c | 26 | 17.8 | 84.8 | 122070 | 12 | AC175643 | AC175643 Loxodonta |
| c | 27 | 17.8 | 84.8 | 123124 | 12 | AC151512 | AC151512 Dasypus n |
| c | 28 | 17.8 | 84.8 | 138173 | 12 | AC151513 | AC151513 Dasypus n |
| c | 29 | 17.8 | 84.8 | 139177 | 5 | AC097060 | AC097060 Homo sapi |
| c | 30 | 17.8 | 84.8 | 141201 | 12 | AC022637 | AC022637 Homo sapi |
| | 31 | 17.8 | 84.8 | 141741 | 5 | AC090329 | AC090329 Homo sapi |
| c | 32 | 17.8 | 84.8 | 141860 | 4 | AP004126 | AP004126 Oryza sat |
| c | 33 | 17.8 | 84.8 | 147178 | 12 | AC026014 | AC026014 Homo sapi |
| | 34 | 17.8 | 84.8 | 153099 | 12 | AC149983 | AC149983 Strongylo |
| | 35 | 17.8 | 84.8 | 155797 | 12 | AC073049 | AC073049 Homo sapi |
| c | 36 | 17.8 | 84.8 | 157466 | 11 | AL928852 | AL928852 Zebrafish |
| | 37 | 17.8 | 84.8 | 157606 | 5 | AC090897 | AC090897 Homo sapi |
| c | 38 | 17.8 | 84.8 | 162117 | 6 | AC140270 | AC140270 Mus muscu |
| | 39 | 17.8 | 84.8 | 162911 | 5 | AC073486 | AC073486 Homo sapi |
| | 40 | 17.8 | 84.8 | 164878 | 12 | CT025582 | CT025582 Danio rer |
| | 41 | 17.8 | 84.8 | 168473 | 11 | BX649544 | BX649544 Zebrafish |
| c | 42 | 17.8 | 84.8 | 169092 | 12 | AC027572 | AC027572 Homo sapi |
| c | 43 | 17.8 | 84.8 | 172209 | 12 | CR936422 | CR936422 Danio rer |
| c | 44 | 17.8 | 84.8 | 173539 | 11 | CR456632 | CR456632 Zebrafish |
| | 45 | 17.8 | 84.8 | 176167 | 5 | AC096656 | AC096656 Homo sapi |
| c | 46 | 17.8 | 84.8 | 178875 | 12 | AP001567 | AP001567 Homo sapi |
| c | 47 | 17.8 | 84.8 | 180130 | 12 | AC159714 | AC159714 Mus muscu |
| | 48 | 17.8 | 84.8 | 181361 | 12 | AC015571 | AC015571 Homo sapi |
| c | 49 | 17.8 | 84.8 | 183466 | 5 | AP005241 | AP005241 Homo sapi |
| | 50 | 17.8 | 84.8 | 185726 | 12 | AC174686 | AC174686 Bos tauru |

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OM nucleic - nucleic search, using sw model

Run on:          May 26, 2006, 04:26:31 ; Search time 70.6718 Seconds
                                                (without alignments)
                                           2071.790 Million cell updates/sec


Title:           US-10-718-955-7
Perfect score:   21
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        5244920 seqs, 3486124231 residues


Total number of hits satisfying chosen parameters:       10489840


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries


Database :       N_Geneseq_8:*
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        Pred. No. is the number of results predicted by chance to have a
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        and is derived by analysis of the total score distribution.


                            SUMMARIES

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     3   16.8   80.0  35089  14  AED76241              Aed76241 Human CA
     4   16.8   80.0  64482  12  ADQ59515              Adq59515 Human can
     5   16.8   80.0  64482  14  ADZ13896              Adz13896 Murine ca
     6   16.8   80.0 127602  14  AEA61155              Aea61155 Human GLU
     7   16.4   78.1    334   9  ACL19379              Acl19379 DNA clone

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| c | 8 | 16.2 | 77.1 | 336 | 6 | ABL84872 | Abl84872 Human ova |
| | 9 | 16.2 | 77.1 | 429 | 4 | AAK75496 | Aak75496 Human imm |
| c | 10 | 16.2 | 77.1 | 530 | 5 | ABV46429 | Abv46429 Human pro |
| | 11 | 16.2 | 77.1 | 551 | 9 | ACH41900 | Ach41900 Human foe |
| | 12 | 16.2 | 77.1 | 961 | 14 | AEB67705 | Aeb67705 Rice geno |
| | 13 | 16.2 | 77.1 | 1041 | 5 | ABA17818 | Aba17818 Human ner |
| | 14 | 16.2 | 77.1 | 1042 | 5 | ABA17819 | Aba17819 Human ner |
| | 15 | 16.2 | 77.1 | 1042 | 5 | ABA17820 | Aba17820 Human ner |
| | 16 | 16.2 | 77.1 | 1076 | 6 | ABZ70862 | Abz70862 Human ATP |
| c | 17 | 16.2 | 77.1 | 1492 | 3 | AAA51403 | Aaa51403 Chromosom |
| c | 18 | 16.2 | 77.1 | 1749 | 6 | ABL90045 | Abl90045 Human pol |
| | 19 | 16.2 | 77.1 | 1850 | 3 | AAZ33320 | Aaz33320 Human sec |
| | 20 | 16.2 | 77.1 | 1902 | 2 | AAV52612 | Aav52612 Nucleotid |
| | 21 | 16.2 | 77.1 | 1902 | 2 | AAV52611 | Aav52611 Nucleotid |
| | 22 | 16.2 | 77.1 | 2332 | 10 | ADA53832 | Ada53832 Human cod |
| | 23 | 16.2 | 77.1 | 2780 | 4 | AAK94287 | Aak94287 Human ful |
| | 24 | 16.2 | 77.1 | 2780 | 12 | ADL30899 | Adl30899 Full leng |
| | 25 | 16.2 | 77.1 | 2925 | 3 | AAA75156 | Aaa75156 cDNA enco |
| | 26 | 16.2 | 77.1 | 3025 | 10 | ADC42880 | Adc42880 REMAP enc |
| c | 27 | 16.2 | 77.1 | 3046 | 4 | AAH54418 | Aah54418 S. epider |
| | 28 | 16.2 | 77.1 | 3751 | 11 | AEA90321 | Aea90321 Human NOV |
| | 29 | 16.2 | 77.1 | 14789 | 4 | ABL29350 | Abl29350 Drosophil |
| | 30 | 16.2 | 77.1 | 40085 | 14 | AEA61140 | Aea61140 Human FMO |
| | 31 | 16.2 | 77.1 | 103738 | 14 | ADX06943 | Adx06943 Cyclin-de |
| c | 32 | 16.2 | 77.1 | 110000 | 5 | AAI61373_0 | Aai61373 Soybean 3 |
| | 33 | 16.2 | 77.1 | 171398 | 14 | ADZ13359 | Adz13359 Human can |
| | 34 | 16.2 | 77.1 | 191584 | 13 | ABD33586 | Abd33586 Human can |
| | 35 | 16.2 | 77.1 | 191584 | 13 | ADR67026 | Adr67026 Human can |
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| | 37 | 16 | 76.2 | 402 | 13 | ACF90718 | Acf90718 Human SIR |
| c | 38 | 16 | 76.2 | 1933 | 14 | AEB35306 | Aeb35306 Human Gef |
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| c | 40 | 15.8 | 75.2 | 52 | 8 | ACC79604 | Acc79604 Skp gene |
| c | 41 | 15.8 | 75.2 | 52 | 10 | ADE29212 | Ade29212 Multivale |
| c | 42 | 15.8 | 75.2 | 52 | 12 | ADM32738 | Adm32738 PCR prime |
| | 43 | 15.8 | 75.2 | 185 | 9 | ACL19389 | Acl19389 DNA clone |
| | 44 | 15.8 | 75.2 | 286 | 10 | ABX82684 | Abx82684 Corn ear- |
| | 45 | 15.8 | 75.2 | 342 | 9 | ACL19391 | Acl19391 DNA clone |
| | 46 | 15.8 | 75.2 | 357 | 9 | ACL19394 | Acl19394 DNA clone |
| c | 47 | 15.8 | 75.2 | 373 | 2 | AAQ43724 | Aaq43724 Sequence |
| c | 48 | 15.8 | 75.2 | 373 | 2 | AAX16669 | Aax16669 Bovine Y |
| | 49 | 15.8 | 75.2 | 531 | 9 | ACL19386 | Acl19386 DNA clone |
| | 50 | 15.8 | 75.2 | 548 | 9 | ACL19385 | Acl19385 DNA clone |
| | 51 | 15.8 | 75.2 | 549 | 9 | ACL19381 | Acl19381 DNA clone |
| | 52 | 15.8 | 75.2 | 567 | 9 | ACL19392 | Acl19392 DNA clone |
| | 53 | 15.8 | 75.2 | 573 | 9 | ACL19383 | Acl19383 DNA clone |
| c | 54 | 15.8 | 75.2 | 577 | 10 | AAD50050 | Aad50050 Human fat |
| | 55 | 15.8 | 75.2 | 592 | 9 | ACL19393 | Acl19393 DNA clone |
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   GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on:          May 26, 2006, 04:56:26 ; Search time 20.0898 Seconds
                                           (without alignments)
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Sequence:        1 cactctttcctatgtatatgc 21


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        1403666 seqs, 935554401 residues


Total number of hits satisfying chosen parameters:      2807332


Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
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|   | 19 | 16.2 | 77.1 | 91831  | 3 | US-09-949-016-13694 | Sequence 13694, A    |
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|   | 38 | 15.8 | 75.2 | 3383   | 3 | US-08-884-324-12    | Sequence 12, Appl    |
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| c | 44 | 15.8 | 75.2 | 3879   | 3 | US-10-060-506-35    | Sequence 35, Appl    |
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OM nucleic - nucleic search, using sw model

Run on:          May 26, 2006, 05:16:51 ; Search time 132.762 Seconds
                                          (without alignments)
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Sequence:        1 cactctttcctatgtatatgc 21


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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| c | 15 | 17.4 | 82.9 | 680    | 7  | US-10-027-632-133109   | Sequence 133109,     |
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OM nucleic - nucleic search, using sw model

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Sequence:        1 cactctttcctatgtatatgc 21


Scoring table:   IDENTITY_NUC
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Searched:        242596 seqs, 56442199 residues


Total number of hits satisfying chosen parameters:       485192


Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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| c | 30 | 14.2 | 67.6 | 534 | 7 | US-11-217-529-76 | Sequence 76, Appl |
| | 31 | 14.2 | 67.6 | 553 | 6 | US-10-488-619-1138 | Sequence 1138, Ap |
| c | 32 | 14.2 | 67.6 | 577 | 6 | US-10-488-619-1139 | Sequence 1139, Ap |
| | 33 | 14.2 | 67.6 | 903 | 7 | US-11-217-529-3323 | Sequence 3323, Ap |
| c | 34 | 14.2 | 67.6 | 1383 | 6 | US-10-953-349-11043 | Sequence 11043, A |
| | 35 | 14.2 | 67.6 | 1431 | 7 | US-11-217-529-3429 | Sequence 3429, Ap |
| | 36 | 14.2 | 67.6 | 1437 | 7 | US-11-217-529-78974 | Sequence 78974, A |
| | 37 | 14.2 | 67.6 | 1776 | 6 | US-10-953-349-2115 | Sequence 2115, Ap |
| c | 38 | 14.2 | 67.6 | 1866 | 7 | US-11-217-529-148 | Sequence 148, App |
| c | 39 | 14.2 | 67.6 | 2007 | 7 | US-11-293-697-1897 | Sequence 1897, Ap |
| c | 40 | 14.2 | 67.6 | 2589 | 7 | US-11-217-529-78347 | Sequence 78347, A |
| | 41 | 14.2 | 67.6 | 3381 | 7 | US-11-293-697-1123 | Sequence 1123, Ap |
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| c | 57 | 13.8 | 65.7 | 1296 | 7 | US-11-217-529-173598 | Sequence 173598, |
| | 58 | 13.8 | 65.7 | 1678 | 6 | US-10-953-349-11625 | Sequence |

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OM nucleic - nucleic search, using sw model

Run on:         May 26, 2006, 04:39:39 ; Search time 454.588 Seconds
                                          (without alignments)
                                         2583.230 Million cell updates/sec


Title:          US-10-718-955-7
Perfect score:  21
Sequence:       1 cactctttcctatgtatatgc 21


Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0


Searched:       48236798 seqs, 27959665780 residues


Total number of hits satisfying chosen parameters:      96473596


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries


Database :      EST:*
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                13:  gb_gss3:*
                14:  gb_gss4:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                     %
Result              Query
   No.     Score   Match Length DB   ID                            Description
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       1      21   100.0    684  12  CE798192             CE798192 tigr-gss-
       2      21   100.0    724  12  CE773639             CE773639 tigr-gss-
       3    18.4    87.6    500  12  CE708194             CE708194 tigr-gss-
       4    18.4    87.6    631   2  BJ824737          BJ824737 BJ824737
  c    5    18.4    87.6    671  14  AG178927             AG178927 Pan trogl
  c    6      18    85.7    517  13  CL355721             CL355721 RPCI44_41
       7      18    85.7    620  11  BZ179705             BZ179705 CH230-484
  c    8    17.8    84.8    225  11  BH228958             BH228958 1006149D1
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|   | 20  | 17.8 | 84.8 | 898  | 5  | CK418265 | CK418265 AUF_IpInt |
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|   | 23  | 17.4 | 82.9 | 399  | 12 | CE569004 | CE569004 tigr-gss-  |
| c | 24  | 17.4 | 82.9 | 416  | 1  | AA724080 | AA724080 ah98g09.s |
| c | 25  | 17.4 | 82.9 | 422  | 11 | AQ030469 | AQ030469 HS_2183_A |
|   | 26  | 17.4 | 82.9 | 456  | 11 | BH338663 | BH338663 CH230-194 |
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|   | 29  | 17.4 | 82.9 | 520  | 14 | DX234758 | DX234758 OR_ABa011 |
|   | 30  | 17.4 | 82.9 | 536  | 11 | BH264523 | BH264523 CH230-91C |
| c | 31  | 17.4 | 82.9 | 562  | 11 | AQ987060 | AQ987060 RPCI-23-3 |
| c | 32  | 17.4 | 82.9 | 606  | 12 | CE473448 | CE473448 tigr-gss-  |
| c | 33  | 17.4 | 82.9 | 714  | 14 | AG090255 | AG090255 Pan trogl |
|   | 34  | 17.4 | 82.9 | 780  | 14 | DX189320 | DX189320 OR_ABa005 |
| c | 35  | 17.4 | 82.9 | 826  | 14 | CT247514 | CT247514 Sus scrof |
| c | 36  | 17.4 | 82.9 | 861  | 1  | AL562437 | AL562437 AL562437  |
| c | 37  | 17.4 | 82.9 | 1138 | 12 | CL147276 | CL147276 ISB1-156L |
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|   | 40  | 17   | 81.0 | 524  | 14 | AG249431 | AG249431 Lotus cor |
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|   | 44  | 17   | 81.0 | 677  | 12 | CC769666 | CC769666 CH240_134 |
|   | 45  | 17   | 81.0 | 688  | 1  | AJ502427 | AJ502427 AJ502427  |
|   | 46  | 17   | 81.0 | 711  | 3  | BU460510 | BU460510 603777237 |
| c | 47  | 17   | 81.0 | 751  | 10 | DR916445 | DR916445 EST110798 |
|   | 48  | 17   | 81.0 | 843  | 14 | CT283381 | CT283381 Sus scrof |
| c | 49  | 17   | 81.0 | 861  | 10 | DT740848 | DT740848 EST117469 |
|   | 50  | 17   | 81.0 | 887  | 14 | CT398723 | CT398723 Sus scrof |
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| c | 52  | 17   | 81.0 | 934  | 14 | CNS00C4O | AL058421 Drosophil |
| c | 53  | 17   | 81.0 | 957  | 10 | DR931355 | DR931355 EST112289 |

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OM nucleic - nucleic search, using sw model

Run on:            May 26, 2006, 04:36:41 ; Search time 195.957 Seconds
                                            (without alignments)
                                            6853.025 Million cell updates/sec

Title:             US-10-718-955-8
Perfect score:     21
Sequence:          1 cgatttaaggggcaagttagc 21

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:       12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries

Database :         GenEmbl:*
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                   12:  gb_htg:*
                   13:  gb_in:*
                   14:  gb_om:*
                   15:  gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
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SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
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|   | 1 | 17.8 | 84.8 | 65013 | 12 | AC163822 | AC163822 Bos tauru |
| c | 2 | 17.4 | 82.9 | 153019 | 6 | AC120156 | AC120156 Mus muscu |
| c | 3 | 17.4 | 82.9 | 165328 | 5 | AC022929 | AC022929 Homo sapi |
|   | 4 | 17.4 | 82.9 | 174690 | 12 | AC163941 | AC163941 Bos tauru |
| c | 5 | 17.4 | 82.9 | 203641 | 6 | AL845297 | AL845297 Mouse DNA |
|   | 6 | 17.4 | 82.9 | 214941 | 12 | AC150409 | AC150409 Branchios |
| c | 7 | 17 | 81.0 | 154025 | 12 | AC142058 | AC142058 Rattus no |

|   |    |      |      |        |    |          |                     |
|---|----|------|------|--------|----|----------|---------------------|
|   | 8  | 17   | 81.0 | 177071 | 12 | AC128090 | AC128090 Rattus no  |
| c | 9  | 17   | 81.0 | 214241 | 12 | AC157426 | AC157426 Bos tauru  |
| c | 10 | 17   | 81.0 | 229506 | 12 | AC160328 | AC160328 Bos tauru  |
| c | 11 | 17   | 81.0 | 252738 | 12 | AC159838 | AC159838 Bos tauru  |
|   | 12 | 16.8 | 80.0 | 344    | 4  | AF035390 | AF035390 Armillari  |
|   | 13 | 16.8 | 80.0 | 101682 | 12 | AC091468 | AC091468 Mus muscu  |
| c | 14 | 16.8 | 80.0 | 130665 | 6  | AF289666 | AF289666 Mus muscu  |
|   | 15 | 16.8 | 80.0 | 138507 | 6  | AC120390 | AC120390 Mus muscu  |
|   | 16 | 16.8 | 80.0 | 150795 | 12 | AC168182 | AC168182 Muntiacus  |
|   | 17 | 16.8 | 80.0 | 150851 | 11 | BX927068 | BX927068 Zebrafish  |
| c | 18 | 16.8 | 80.0 | 154561 | 5  | AC021355 | AC021355 Homo sapi  |
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|   | 21 | 16.8 | 80.0 | 170072 | 6  | AC116329 | AC116329 Mus muscu  |
|   | 22 | 16.8 | 80.0 | 177225 | 4  | BX908808 | BX908808 Neurospor  |
|   | 23 | 16.8 | 80.0 | 179404 | 12 | AC175756 | AC175756 Bos tauru  |
| c | 24 | 16.8 | 80.0 | 179790 | 6  | AC167419 | AC167419 Mus muscu  |
|   | 25 | 16.8 | 80.0 | 182945 | 12 | AC141518 | AC141518 Rattus no  |
|   | 26 | 16.8 | 80.0 | 183318 | 6  | AL844856 | AL844856 Mouse DNA  |
| c | 27 | 16.8 | 80.0 | 185786 | 12 | AC079372 | AC079372 Mus muscu  |
|   | 28 | 16.8 | 80.0 | 191322 | 6  | AC140314 | AC140314 Mus muscu  |
|   | 29 | 16.8 | 80.0 | 195225 | 12 | AC023930 | AC023930 Homo sapi  |
|   | 30 | 16.8 | 80.0 | 197774 | 12 | CR626902 | CR626902 Danio rer  |
|   | 31 | 16.8 | 80.0 | 201747 | 12 | AC163876 | AC163876 Bos tauru  |
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| c | 33 | 16.8 | 80.0 | 217804 | 12 | AC117297 | AC117297 Rattus no  |
|   | 34 | 16.8 | 80.0 | 223529 | 6  | AC137871 | AC137871 Mus muscu  |
|   | 35 | 16.8 | 80.0 | 224961 | 12 | AC107529 | AC107529 Rattus no  |
| c | 36 | 16.8 | 80.0 | 235976 | 12 | AC119627 | AC119627 Rattus no  |
|   | 37 | 16.8 | 80.0 | 245942 | 12 | AC121374 | AC121374 Rattus no  |
|   | 38 | 16.8 | 80.0 | 246613 | 12 | AC161077 | AC161077 Bos tauru  |
| c | 39 | 16.8 | 80.0 | 248528 | 12 | AC095666 | AC095666 Rattus no  |
|   | 40 | 16.8 | 80.0 | 250578 | 12 | AC173126 | AC173126 Bos tauru  |
|   | 41 | 16.8 | 80.0 | 254581 | 12 | AC097817 | AC097817 Rattus no  |
| c | 42 | 16.8 | 80.0 | 268268 | 12 | AC129154 | AC129154 Rattus     |

# SCORE Search Results Details for Application 10
# 10-718-955-8.200hits.

This page gives you Search Results detail for the Application 10718955 and Search Result us-10-7:
start | next page

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                          GenCore version 5.1.8
                Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          May 26, 2006, 04:36:41 ; Search time 195.957 Seconds
                                          (without alignments)
                                          6853.025 Million cell updates/sec

Title:           US-10-718-955-8
Perfect score:   21
Sequence:        1 cgatttaaggggcaagttagc 21

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 600 summaries

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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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SUMMARIES

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| | 4 | 17.4 | 82.9 | 174690 | 12 | AC163941 | AC163941 Bos tauru |
| c | 5 | 17.4 | 82.9 | 203641 | 6 | AL845297 | AL845297 Mouse DNA |
| | 6 | 17.4 | 82.9 | 214941 | 12 | AC150409 | AC150409 Branchios |
| c | 7 | 17 | 81.0 | 154025 | 12 | AC142058 | AC142058 Rattus no |
| | 8 | 17 | 81.0 | 177071 | 12 | AC128090 | AC128090 Rattus no |
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| c | 10 | 17 | 81.0 | 229506 | 12 | AC160328 | AC160328 Bos tauru |
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| | 21 | 16.8 | 80.0 | 170072 | 6 | AC116329 | AC116329 Mus muscu |
| | 22 | 16.8 | 80.0 | 177225 | 4 | BX908808 | BX908808 Neurospor |
| | 23 | 16.8 | 80.0 | 179404 | 12 | AC175756 | AC175756 Bos tauru |
| c | 24 | 16.8 | 80.0 | 179790 | 6 | AC167419 | AC167419 Mus muscu |
| | 25 | 16.8 | 80.0 | 182945 | 12 | AC141518 | AC141518 Rattus no |
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| c | 27 | 16.8 | 80.0 | 185786 | 12 | AC079372 | AC079372 Mus muscu |
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| c | 36 | 16.8 | 80.0 | 235976 | 12 | AC119627 | AC119627 Rattus no |
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| | 53 | 16.4 | 78.1 | 77908 | 5 | AC008609 | AC008609 Homo sapi |
| | 54 | 16.4 | 78.1 | 95484 | 12 | AC015854 | AC015854 Homo sapi |
| c | 55 | 16.4 | 78.1 | 100240 | 6 | AL713968 | AL713968 Mouse DNA |
| c | 56 | 16.4 | 78.1 | 102564 | 5 | AC015916 | AC015916 Homo sapi |

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OM nucleic - nucleic search, using sw model

Run on:            May 26, 2006, 04:56:26 ; Search time 20.0898 Seconds
                                              (without alignments)
                                              1955.884 Million cell updates/sec


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Perfect score:     21
Sequence:          1 cgatttaaggggcaagttagc 21


Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0


Searched:          1403666 seqs, 935554401 residues


Total number of hits satisfying chosen parameters:       2807332


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.


                                    SUMMARIES

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| | 7 | 15.4 | 73.3 | 601 | 3 | US-09-949-016-192231 | Sequence 192231, |
| | 8 | 15.4 | 73.3 | 672 | 5 | US-09-974-300-5192 | Sequence 5192, Ap |
| | 9 | 15.4 | 73.3 | 921 | 5 | US-09-974-300-5200 | Sequence 5200, Ap |
| | 10 | 15.4 | 73.3 | 42595 | 5 | US-09-984-429-469 | Sequence 469, App |
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|   | 26 | 15.2 | 72.4 |   6596 | 3 | US-09-032-086-11     | Sequence 11, Appl  |
| c | 27 | 15.2 | 72.4 |  13188 | 3 | US-08-961-527-70     | Sequence 70, Appl  |
| c | 28 | 15.2 | 72.4 |  23640 | 3 | US-09-949-016-13646  | Sequence 13646, A  |
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|   | 30 | 15.2 | 72.4 |  30221 | 3 | US-09-949-016-12577  | Sequence 12577, A  |
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|   | 32 | 15.2 | 72.4 |  78649 | 3 | US-09-949-016-14619  | Sequence 14619, A  |
|   | 33 | 15.2 | 72.4 |  78649 | 3 | US-09-949-016-14620  | Sequence 14620, A  |
|   | 34 | 15.2 | 72.4 |  78649 | 3 | US-09-949-016-16227  | Sequence 16227, A  |
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| c | 41 | 15.2 | 72.4 | 305491 | 3 | US-09-949-016-17550  | Sequence 17550, A  |
|   | 42 | 15.2 | 72.4 | 312470 | 3 | US-09-949-016-14043  | Sequence 14043, A  |
|   | 43 | 15.2 | 72.4 | 336024 | 3 | US-09-949-016-12373  | Sequence 12373, A  |
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| c | 54 | 15   | 71.4 | 385136 | 3 | US-09-949-016-16073  | Sequence 16073     |

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OM nucleic - nucleic search, using sw model

Run on:         May 26, 2006, 05:18:23 ; Search time 4.03096 Seconds
                                          (without alignments)
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0


Searched:       242596 seqs, 56442199 residues


Total number of hits satisfying chosen parameters:      485192


Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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        Pred. No. is the number of results predicted by chance to have a
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  c     6    14.6   69.5   1850   6  US-10-953-349-16973      Sequence 16973, A
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        9    14.4   68.6   1355   6  US-10-953-349-25095      Sequence 25095, A
       10    14.4   68.6   3414   7  US-11-217-529-79249      Sequence 79249, A
       11    14.2   67.6    423   7  US-11-217-529-79945      Sequence 79945, A
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  c    13    14.2   67.6    576   6  US-10-953-349-7850       Sequence 7850, Ap
       14    14.2   67.6    900   6  US-10-953-349-24207      Sequence 24207, A
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|   | 15 | 14.2 | 67.6 | 960  | 7 | US-11-121-154-78     | Sequence 78, Appl      |
|   | 16 | 14.2 | 67.6 | 1403 | 6 | US-10-953-349-31669  | Sequence 31669, A      |
|   | 17 | 14.2 | 67.6 | 1638 | 7 | US-11-217-529-5647   | Sequence 5647, Ap      |
|   | 18 | 14.2 | 67.6 | 1756 | 6 | US-10-953-349-22761  | Sequence 22761, A      |
| c | 19 | 14.2 | 67.6 | 1789 | 7 | US-11-293-697-1953   | Sequence 1953, Ap      |
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OM nucleic - nucleic search, using sw model

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                                              (without alignments)
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Scoring table:      IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched:           48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:       96473596

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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          Pred. No. is the number of results predicted by chance to have a
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                                    SUMMARIES

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| c | 5 | 17.4 | 82.9 | 435 | 9 | DN168287 | DN168287 LH__Ea03B |
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| c | 7 | 17.4 | 82.9 | 727 | 14 | AG431543 | AG431543 Mus muscu |
| c | 8 | 17.4 | 82.9 | 940 | 14 | DU741343 | DU741343 APKI660.b |

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| c | 9 | 17 | 81.0 | 616 | 7 | AV780588 | AV780588 AV780588 |
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| c | 11 | 16.8 | 80.0 | 297 | 8 | CV623541 | CV623541 L_AH-aaa2 |
| | 12 | 16.8 | 80.0 | 347 | 4 | BY145940 | BY145940 BY145940 |
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| | 15 | 16.8 | 80.0 | 355 | 4 | BY775556 | BY775556 BY775556 |
| | 16 | 16.8 | 80.0 | 358 | 4 | BY788876 | BY788876 BY788876 |
| | 17 | 16.8 | 80.0 | 368 | 4 | BY131922 | BY131922 BY131922 |
| | 18 | 16.8 | 80.0 | 368 | 4 | BY773684 | BY773684 BY773684 |
| | 19 | 16.8 | 80.0 | 370 | 4 | BY766589 | BY766589 BY766589 |
| | 20 | 16.8 | 80.0 | 392 | 5 | CD702231 | CD702231 EST18755 |
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| | 46 | 16.8 | 80.0 | 735 | 14 | DE132933 | DE132933 Oryzias l |
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| | 48 | 16.8 | 80.0 | 787 | 3 | BU425942 | BU425942 |

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OM nucleic - nucleic search, using sw model

Run on:            May 26, 2006, 04:56:26 ; Search time 268.82 Seconds
                                            (without alignments)
                                            1955.884 Million cell updates/sec


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Scoring table:     IDENTITY_NUC
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Total number of hits satisfying chosen parameters:      2807332


Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 600 summaries


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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


                                 SUMMARIES
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|   | Result No. | Score | % Query Match | Length | DB | ID | Description |
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|   | 6 | 64.2 | 22.8 | 767677 | 3 | US-09-949-016-12147 | Sequence 12147, A |
|   | 7 | 64.2 | 22.8 | 767677 | 3 | US-09-949-016-17361 | Sequence 17361, A |
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|   | 27 | 58   | 20.6 | 72048  | 3 | US-09-949-002-600   | Sequence 600, App  |
|   | 28 | 58   | 20.6 | 72048  | 3 | US-09-949-002-684   | Sequence 684, App  |
|   | 29 | 57.6 | 20.5 | 601    | 3 | US-09-949-002-5378  | Sequence 5378, Ap  |
|   | 30 | 57.4 | 20.4 | 87648  | 3 | US-09-949-016-13655 | Sequence 13655, A  |
|   | 31 | 57.2 | 20.4 | 304533 | 3 | US-09-949-016-15371 | Sequence 15371, A  |
|   | 32 | 57.2 | 20.4 | 304533 | 3 | US-09-949-016-15372 | Sequence 15372, A  |
|   | 33 | 57   | 20.3 | 601    | 3 | US-09-949-016-31837 | Sequence 31837, A  |
|   | 34 | 57   | 20.3 | 601    | 3 | US-09-949-016-40022 | Sequence 40022, A  |
|   | 35 | 57   | 20.3 | 601    | 3 | US-09-949-016-74004 | Sequence 74004, A  |
|   | 36 | 57   | 20.3 | 601    | 3 | US-09-949-016-74110 | Sequence 74110, A  |
|   | 37 | 57   | 20.3 | 1016   | 2 | US-08-109-391A-3    | Sequence 3, Appli  |
|   | 38 | 57   | 20.3 | 1016   | 2 | US-08-459-019A-3    | Sequence 3, Appli  |
|   | 39 | 57   | 20.3 | 1016   | 2 | US-08-460-428A-3    | Sequence 3, Appli  |
|   | 40 | 57   | 20.3 | 1016   | 3 | US-08-458-860A-3    | Sequence 3, Appli  |
|   | 41 | 57   | 20.3 | 1016   | 3 | US-09-196-447B-3    | Sequence 3, Appli  |
| c | 42 | 57   | 20.3 | 69813  | 3 | US-09-949-016-12455 | Sequence 12455, A  |
| c | 43 | 57   | 20.3 | 69813  | 3 | US-09-949-016-13905 | Sequence 13905, A  |
| c | 44 | 57   | 20.3 | 69813  | 3 | US-09-949-016-13906 | Sequence 13906, A  |
| c | 45 | 57   | 20.3 | 69833  | 3 | US-09-949-016-12861 | Sequence 12861, A  |
|   | 46 | 56.8 | 20.2 | 601    | 3 | US-09-949-016-57872 | Sequence 57872, A  |
|   | 47 | 56.8 | 20.2 | 236474 | 3 | US-09-949-016-13418 | Sequence 13418, A  |
| c | 48 | 56.6 | 20.1 | 4084   | 3 | US-08-866-340-1     | Sequence 1, Appli  |
| c | 49 | 56.6 | 20.1 | 4460   | 3 | US-09-103-875-4     | Sequence 4, Appli  |
|   | 50 | 56.4 | 20.1 | 601    | 3 | US-09-949-002-5377  | Sequence 5377, Ap  |